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Claims

1. Protein L having the ability to bind to the light chains of immunoglobulins, characterized in that the protein L has the following amino acid sequence:

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	Ala 1		Glu	Asņ	Lys 5	Glu	Glu	Thr	Pro	Glu 10	Thr	Pro	Glu	Thr	Asp 15	Ser
	Glu	Glu	Glu	Val 20	Thr	Ile	Lys	Ala	Asn 25	Leu	Ile	Phe	Ala	Asn 30	Gly	Ser
10	Thr	Gln	Thr 35	Ala	Glu	Phe	Lys	Gly 40	Thr	Phe	Glu	Lys	Ala 45	Thr	Ser	Glu
	Ala	Tyr 50	Ala	Tyr	Ala	Asp	Thr 55	Leu	Lys	Lys	Asp	Asn 60	Gly	Glu	Tyr	Thr
15	Val _65	Asp 32	Val	λla	увр	Lys 70	Gly	Tyr	Thr	Leu	Asn 75	Ile	Lys	Phe	Ala	Gly 80
	Lys	Glu	Lys	Thr	Pro 85	Glu	Glu	Pro	Tye	Glu 90	Glu	Val	Thr	Ile	Lys 95	Ala
20	Asn	Leu	Ile	Tyr 100	Ala	Asp	Gly	Lys	Thr. 105	Gln	Thr	Ala	Glu	Phe 110	Lys	Gly
	Thr	Phe	Glu 115	Glu	Ala	Thr	Ala	Glu 120	Ala	Tyr	Arg	Tyr	Ala 125	Asp	Ala	Leu
	Lys	Lys 130	Двр	Asn	Gly	Glu	Tyr 135	Thr	Val		val	Ala 140	Asp	Lys	Gly	Tyr
25	Thr 145	Leu	Asn	Ile	Lys	Phe 150	Ala	Gly			Lys 155	Thr	Pro	Glu	Glu	160
	Lys	Glu	Glu	Val	Thr 165	Ile	Lys	Ala	Asn	Leu 170	Ile	Tyr	Ala	Asp	Gly 175	Lys
3 0	Thr	Gln	Thr	Ala 180	Glu	Phe	Lys	Gly	Thr 185	Phe	Glu	Glu	Ala	190	Ala	Glu
	Ala	Tyr	Arg 195	Tyr	Ala	Asp	Leu	Leu 200	Ala	Lys	Glu	Asn	Gly 205	Lye	ту	Thr
2.5	Val	Asp 210	Val	Ala	Asp	Lys	Gly 215	туr	Thr	Leu	Asn	11e 220	Lys	; Phe	e Ala	a Gly

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		— в4														
	Lys 225	Glu	Lys	Thr	Pro	Glu 230	Glu	Pro	Lys	Glu	Glu 235	Val	Thr	Ile	Lys	Ala 240
5	λsn	Leu	Ile	Tyr	Ala 245	ysb	Gly	Lys	Thr	Gln 250	Thr	Ala	Glu	Phe	Lys 255	Gly
	Thr	Phe	Ala	Glu 260	Ala	Thr	Ala	Glu	Ala 265	Tyr	Arg	Tyr	Ala	Asp 270	Leu	Leu
10	λla	Lys	Glu 275		Gly	Lys	Tyr	Thr 280	Λla — · E	Asp 35	Leu	Glu	Asp 285	Gly	Gly	Tyr
	Thr	Ile 290	λsn	Ile	λrg	Phe	λla 295	Gly	Lys	Lys	Val	300 ysb	Glu	Lys	Pro	Glu
	Glu		-													

- and variants, subfragments, multiples or mixtures of the domains B1-B5 having the same binding properties.
- DNA-sequence, characterized in that
 it codes for the protein according to Claim 1 and has
 the following nucleotide sequence:

GCG GTA GAA AAT AAA GAA GAA ACA CCA GAA ACA CCA GAA ACT GAT TCA <u>-</u>8 GAA GAA GAA GTA ACA ATC AAA GCT AAC CTA ATC TTT GCA AAT GGA AGC 96 ACA CAA ACT GCA GAA TTC AAA GGA ACA TTT GAA AAA GCA ACA TCA GAA 144 GCT TAT GCG TAT GCA GAT ACT TTG AAG AAA GAC AAT GGA GAA TAT ACT 192 GTA GAT GTT GCA GAT AAA GGT TAT ACT TTA AAT ATT AAA TTT GCT GGA 240 30 288 AAC TTA ATC TAT GCA GAT GGA AAA ACA CAA ACA GCA GAA TTC AAA GGA 336 ACA TTT GAA GAA GCA ACA GCA GAA GCA TAC AGA TAT GCA GAT GCA TTA 384 35 AAG AAG GAC AAT GGA GAA TAT ACA GTA GAC GTT GCA GAT AAA GGT TAT 432 -ACT TTA AAT ATT AAA TTT GCT GGA AAA GAA AAA ACA CCA GAA GAA CCA 480 AAA GAA GAA GTT ACT ATT AAA GCA AAC TTA ATC TAT GCA GAT GGA AAA 528

15	GAA	TAAT	'AA														921
	ACT	ATT	AAT	ATT	AGA	TTT	GCA	GGT	AAG	AAA	GTT	GAC	GAA	AAA	CCA	GAA .	912
	GCA	AAA	GAA	AAT	GGT	AAA	TAT	ACA	GCA	GAC	TTA	GAA	GAT	GGT	GG <u>A</u>	TAC	864
10	ACA	TTT	GCA	GAA	GCA	ACA	GCA	GAA	GCA	TAC	AGA	TAC	GCT	GAC	TTA	TTA	816
	AAC	TTA	ATC	TAT	GCA	GAT	GGA	AAA	ACT	CAA	ACA	GCA	GAG	TTC	AAA	GGA	768
	AAA	GAA	AAA	ACA	CCA	GAA	GAA	CCA	AAA	GAA	GAA	GTT	ACT	ATT	AAA	GCA	720
5	GTA	GAC	GTT	GCA	GAT	AAA	GGT	TAT	ACT	TTA	AAT	ATT	AAA	TTT	GCT	GGA	672
5	GCA	TAC	AGA	TAT	GCT	GAC	TTA	TTA	GCA	AAA	GAA	AAT	GGT	AAA	TAT	ACA	624
	ACA	CAA	ACA	GCA	GAA	TTC	AAA	GGA	ACA	TTT	GAA	GAA	GCA	ACA	GCA	GAA	576

- 3. A hybrid protein, characterized in that it includes one or more of the B1-B5-domains according to Claim 1 which bind to the light chains in immunoglobulins of all classes, and domains which bind to heavy chains in immunoglobulin G.
- 4. A hybrid protein according to Claim 3, c h a r 25 a c t e r i z e d in that the domains which bind to
 heavy chains in immunoglobulin G are chosen from among
 the C1- and C2-domains in protein G or from among any
 other functionally similar proteins which bind to heavy
 chains in immunoglobulin G, and variants, subfragments,
 30 multiples or mixtures thereof having the same binding
 properties.
- 5. A hybrid protein according to Claim 4, c h a r a c t e r i z e d in that the hybrid protein has the following amino acid sequence:

	Al	a ∵a i ·	1 G1	u As:	n Lys 5		Glu	Thr	Pro	Glu 10	Thr	Pro	Glu	Thr	Asp	Ser
5	Gl	u Gl	u Glu	ı Val 20		Ile	Lys	Ala	Asn 25	Leu	Ile	Phe	Ala	Asn 30	Gly	Ser
	Th	r Gli	n Thi		Glu	Phe	Lys	Gly 40	Thr	Phe	Glu	Lys	Ala 45	Thr	Ser	Glu
10	Ala	1 Ty:	r Ala	Tyr	Ala	Asp	Thr 55	Leu	Lys	Lys	Asp	Asn 60	Gly	Glu	Tyr	Thr
	Val 65		Val	Ala	Asp	Lys 70	Gly	Tyr	Thr	Leu	Asn 75	Ile	Lys	Phe	Ala	Gly 80
15	Lys	Glu	Lys	Thr	Pro 85	Glu	Glu	Pro	Lys	Glu 90	Glu	Val	Thr	Ile	Lys 95	Ala
	Asn	Leu	Ile	Tyr 100	Ala	Asp	Gly	Lys	Thr 105	Gln	Thr	Ala	Glu	Phe 110	Lys	Gly
20	Thr	Phe	Glu 115	Glu	Ala	Thr	Ala	Glu 120	Ala	Tyr	Arg	Tyr	Ala 125	Asp	Ala	Leu
	Lys	Lys 130	Asp	Asn	Gly	Glu	Tyr 135	Thr	Val	Asp	Val	Ala 140	Asp	Lys	Gly	Tyr
	Thr 145	Leu	Asn	Ile	Lys	Phe 150	Ala	Gly	Lys	Glu	Lys 155	Thr	Pro	Glu	Glu	Pro 160
25	Lys	Glu	Glu	Val	Thr 165	Ile	Lys	Ala	Asn	Leu 170	Ile	Tyr	Ala	Asp	Gly 175	Lys
	Thr	Gln	Thr	Ala 180	Glu	Phe	Lys	Gly	Thr 185	Phe	Glu	Glu	Ala	Thr 190	Ala	Glu
30	Ala	Tyr	Arg 195	Tyr	Ala	Asp	Leu	Leu 200	Ala	Lys	Glu	Asn	Gly 205		Tyr	Thr
		Asp 210	Val	Ala	Asp	Lys	Gly 215	Tyr	Thr	Leu	Asn	Ile 220	Lys	Phe	Ala	Gly
	Lys 225	Glu	Lys	Thr		Glu 230	Glu	Pro	Lys	Glu	Glu 235	Val	Thr	Ile	Lys	Ala 240
35	Asn	Leu	Ile		Ala 245	Asp	Gly	Lys	Thr	Gln 250	Thr	Ala	Glu	Phe	Lys 255	Gly

- Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu 260 265 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr 5 280 Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu Glu Pro Met Asp Thr Tyr Lys Leu Ile Leu Ash Gly Lys Thr Leu Lys 10 310 Gly Glu Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr 350 340 345 15 Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile 360 Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile 375 20 Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala 395 385 Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val 410 405 Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr 25 425 420 Glu Met
- and variants, subfragments, multiples or mixtures of the domains B1-B5 having the same binding properties.
- 6. DNA-sequence, characterized in that it codes for a protein according to Claim 5 and has the following nucleotide sequence:

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GCG GTA GAA AAT AAA GAA GAA ACA CCA GAA ACA CCA GAA ACT GAT TCA ∔8ે GAA GAA GAA GTA ACA ATC AAA GCT AAC CTA ATC TTT GCA AAT GGA AGC ACA CAA ACT GCA GAA TTC AAA GGA ACA TTT GAA AAA GCA ACA TCA GAA GCT TAT GCG TAT GCA GAT ACT TTG AAG AAA GAC AAT GGA GAA TAT ACT 192 GTA GAT GTT GCA GAT AAA GGT TAT ACT TTA AAT ATT AAA TTT GCT GGA 240 288 AAC TTA ATC TAT GCA GAT GGA AAA ACA CAA ACA GCA GAA TTC AAA GGA 336 ACA TTT GAA GAA GCA ACA GCA GAA GCA TAC AGA TAT GCA GAT GCA TTA 384 10 AAG AAG GAC AAT GGA GAA TAT ACA GTA GAC GTT GCA GAT AAA GGT TAT 432 ACT TTA AAT ATT AAA TTT GCT GGA AAA GAA AAA ACA CCA GAA GAA CCA 480 AAA GAA GAA GTT ACT ATT AAA GCA AAC TTA ATC TAT GCA GAT GGA AAA 528 ACA CAA ACA GCA GAA TTC AAA GGA ACA TTT GAA GAA GCA ACA GCA GAA 15 576 GCA TAC AGA TAT GCT GAC TTA TTA GCA AAA GAA AAT GGT AAA TAT ACA 624 GTA GAC GTT GCA GAT AAA GGT TAT ACT TTA AAT ATT AAA TTT GCT GGA 672 720 AAC TTA ATC TAT GCA GAT GGA AAA ACT CAA ACA GCA GAG TTC AAA GGA 768 ACA TTT GCA GAA GCA ACA GCA GAA GCA TAC AGA TAC GCT GAC TTA TTA 816 . GCA AAA GAA AAT GGT AAA TAT ACA GCA GAC TTA GAA GAT GGT GG<u>A</u> TAC 864 25 ACT ATT AAT ATT AGA TTT GCA GGT AAG AAA GTT GAC GAA AAA CCA GAA 912 GAA CCC ATG GAC ACT TAC AAA TTA ATC CTT AAT GGT AAA ACA TTG AAA 960 GGC GAA ACA ACT ACT GAA GCT GTT GAT GCT ACT GCA GAA AAA GTC 1008 TTC AAA CAA TAC GCT AAC GAC AAC GGT GTT GAC GGT GAA TGG ACT TAC 1056 GAC GAT GCG ACT AAG ACC TTT ACA GTT ACT GAA AAA CCA GAA GTG ATC 1104 GAT GCG TCT GAA TTA ACA CCA GCC GTG ACA ACT TAC AAA CTT GTT ATT 1152 AAT GGT AAA ACA TTG AAA GGC GAA ACA ACT ACT AAA GCA GTA GAC GCA 1200 35 GAA ACT GCA GAA AAA GCC TTC AAA CAA TAC GCT AAC GAC AAC GGT GTT 1248 GAT GGT GTT TGG ACT TAT GAT GCG ACT AAG ACC TTT ACG GTA ACT 1296 1308 GAA ATG TAATAA

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- 7. DNA-sequence, characterized in that it codes for a protein according to Claim 3 and 4.
- 8. DNA-sequence, characterized in that

 it hybridizes to the DNA-sequence of Claim 2, 6 or 7

 under conventional conditions and codes for a protein
 which has the same binding properties as the protein
 according to any one of Claims 1 and 3-5.
- 10 9. A plasmid vector, characterized in that it includes a DNA-sequence according to any one of Claims 2 and 6-8, preferably the vector pHDLG or pHDL.
- 10. A host cell, characterized in that it is transformed with the hybrid plasmid according to Claim 9, in particular a host which belongs to the species <u>E. coli</u>, particularly <u>E. coli</u> LE392, or <u>Bacillus subtilis</u>, <u>Saccaromyces cerevisiae</u>, preferably Id. Ref. DSSM <u>E. coli</u> LE392 pHDL and <u>E. coli</u> LE392/pHDLG respectively.
 - 11. A method for producing a protein according to Claims 1 and 3-5, c h a r a c t e r i z e d by cultivating a host cell according to Claim 10 under suitable conditions; accumulating the protein in the culture or lysing the cells and extracting the protein therefrom.
- 12. A reagent apparatus for binding, separating and identifying immunoglobulins, c.h a r a c t e r i z e d in that it includes a protein according to any one of Claims 1 and 3-5.
- 13. A composition, characterized in that it includes a protein according to any one of Claims 1 and 3-5, and optionally additives or carriers.

14. A pharmaceutical composition, c h a r a c - t e r i z e d in that it includes a protein according to any one of Claims 1 and 3-5, and optionally a pharmaceutically acceptable carrier or extender.